

TABLE 1
 Summary of the results of the BLASTX analysis of the CuraGen database for the identification of protein sequences that may be related to the disease.

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen database	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
1, 2	cg44928667	1090	TGGAGCAGAAAGG TGGAGCTGGACT CCAGG[<i>gap</i>]/TATC TGAGTG[<i>CT</i>]GCGC TGAAGAAATACC AGACTGAGCAA GGAG	gap (1)	TATCT GAGT G(2)	Avg	Lys	Frameshift	kinase receptor	Human Gene SPTREMBL-ID Q60437 INSULIN RECEPTOR TYROSINE KINASE 53 KDA SUBSTRATE-- UNKNOWN, 521 aa	4.60E-246	deletion of 10bp in 3 of 11	17	Metabolic/endocrine/cardiovascular	
3, 4	cg43957213	1529	CATACATAAAGC GGCAAGATTTCAG TCCCTGACCGCA A[<i>gap</i>]/GJGCA- CTTACAGTCTAG TTGGGAAGGGAG ACACAAAT	gap (3)	G (4)			Silent, Non-Coding	muscle channel	Human Gene SWISSPROT-ID P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa [peptide TREMBLNEW-ID P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa [peptide TREMBLNEW-ID E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa		good 10 of 20	1p36.1	Metabolic/endocrine/cardiovascular	Renal Disease
5, 6	cg44912878	1164	ACCGCATCATGG AGGTCATCGATG[T/C]CATCACCAC CACTGCCACAG CCACC	T (5)	C (6)	Ala	Val	CONSERVATIVE	kinase	Human Gene SWISSPROT-ID P17858 6- PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME B) - HOMO SAPIENS (HUMAN), 780 aa		good 2 of 9	21	Metabolic/endocrine/cardiovascular	

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7, 8	cg44912878	3171	CT-A- TCCCTGCCACC TG-CCAGGCCCTCC CTC/GC/GGCTGG TGTCTT-GAGA- CCA-GCCTG- CCAGGCC	G (7)	C (8)			3' UTR	kinase	Human Gene SWISSPROT-ID P17858 6- PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2 7 1 11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME B) - HOMO SAPIENS (HUMAN), 780 aa	good 7 of 20	21		Metabolic/endocrine/cardiovascular		
9, 10	cg44912878	853	ATCATCCAGCTG GGCGGCATATC ATTGGCAGCGCT GCCTTCG/GCIAAG GCCTTTACCACC AGGGAAGGGCG CCGGCAGCGG	CG (9)	GC (10)	Cys	Ser	CONSERVATIVE	kinase	Human Gene SWISSPROT-ID P17858 6- PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2 7 1 11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME B) - HOMO SAPIENS (HUMAN), 780 aa	3.30E-06	good 4 of 8	21		Metabolic/endocrine/cardiovascular	
11, 12	cg44921974	304	TGAGTTCGGTC ACAGACTTGATG TTTTT-GA- AAGC/TJGTAC CAGTTTATTGTCA CCTTCCAACCTGA ACCACTGTCTTG	C (11)	T (12)	Thr	Ala	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC P07148 FATTY ACID-BINDING PROTEIN, LIVER (L-FABP) - Homo sapiens (Human), 127 aa	1.30E-06	9 of 30	2 (4q28)	Metabolic/endocrine/cardiovascular		
13, 14	95124747	643	aaagtggtcttcagagctt ctttccctaatg/c/tlbgg cctcaccatgcaagcang actatttgtagacaa(gaa gcagaagggaaagaagria gg	C (13)	T (14)	Ala	Val	CONSERVATIVE		Calpaectn	1.70E-11	44 of 1050	17		Metabolic/endocrine/cardiovascular	

TABLE 1. BLASTX analysis of the CuraGen sequence

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
15, 16	88073933	751	GGAGTGGGGCTA CGCCAGCCACAA CGGTCTTGACCA CTGGCATGAAC TTTCCAAATGC CAAGGGGGAAA ACCAAGTGGCCCA /GTTGAGCTGCA TACTAAAGACAT CAGGCATGACCC TTCTCTGCAGCC ATGGTC- TGTGTCCTATGAT GGTGG	A (15)	G (16)	Ile	Val	CONSERV ACTIVE		Carbonic Anhydrase 3		5 of 12	8	Metabolic/endocrine/cardiovascular	
17, 18	cg43953338	1246	AATTGGG-TGGT- TTGAAGGATCAC ATAAA- GGAGATCCAGAI A/GA-TGCC- GGCGTTTGATTCT TATTGCTT	A (17)	G (18)			Silent- Coding	synthase	Human Gene Homologous to SWISSPROT-ID P44708 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2 6 1 16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa	3 10E-107	4 of 40	2 (2p13)	Metabolic/endocrine/cardiovascular	
19, 20	cg43953338	3084	ATGTTGGGTATC CTAC- TACTTTGTGTTT CATCTCTCTAAA GTG/G/TTTTTA TTTCCTGTACT GTAGTCCTTTAT TTTAAATGAC	G (19)	T (20)			3' UTR	synthase	Human Gene Homologous to SWISSPROT-ID P44708 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2 6 1 16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa	3 10E-107	4 of 10	2 (2p13)	Metabolic/endocrine/cardiovascular	

TABLE 1. BLASTX analysis of the CuraGen sequence database (version 1.0) for the human gene database (version 1.0) using the BLASTX program (version 2.2.26) with the default parameters. The results are shown in the table below.

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence database	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
21, 22	g42930646	1229	TGTCAGCCCCAC AAATAGGAGTCG TCAATGTTACTG ATCGGGATAGCG TA- TGGATGGAJA/G JTGACGATGAG GAGACCTGCT TCTGCTGAGGAG CTGGAGGACTGG CTGGAGG	A (21)	G (22)	Met	Val	CONSERV ACTIVE	Immun	Human Gene SWISSPROT-ID P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ- BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa	1.80E-198	4 of 19	1	Metabolic/endocrine/cardiovascular	Bone Disease
23, 24	94842816	1303	CCGACGTTCCCT CTTCCACGACT CAGAGCCCACTT A/TITCCACTCT TTGAAACTCCG ACGCGACATCCA ACCGAGCGGT CAGC	A (23)	T (24)	Asn	Lys	NON- CONSERV ACTIVE	Secreted hormone	Adrenomedullin		4 of 55	11	Metabolic/endocrine/cardiovascular	
25, 26	88048627	3294	CCTATTACCAGA GAGGATCGAGCA TGGTCTCTCTCTC C/C/TCTCCACT GTGATCTCTCTG ATCTTTTCTCA TCTTCTGTAGT GGGATGA	C (25)	T (26)	Pro	Ser	NON- CONSERV ACTIVE	Membrane protein	Prion protein (new variant)		2 of 16	20p12.1-13	Metabolic/endocrine/cardiovascular	CNS Disorders
27, 28	88048627	2968	GGTGTCTGACGA GCTGGGGCAGTG GTGGGGGCGCTT GGCGGCTA- C/A/GTGTCTGGGA AGTGCCATGAGC AGGCCCATCATA CATT	A (27)	G (28)			Silent- Coding	Membrane protein	Prion Protein (previously identified variant)		3 of 9	20p12.1-13	Metabolic/endocrine/cardiovascular	CNS Disorders
29, 30	95124747	304	A/gccatcnaatggnaac acgccatggaaccatgat gttaacattcaal[a/c]atcc Bctggggataaggctactt aacaaggaggaccctggaga gtactcatgganaaggag	A (29)	C (30)	Lys	Glu	NON- CONSERV ACTIVE		Calpactin		184 of 350	17	Metabolic/endocrine/cardiovascular	

TABLE 1. BLASTX analysis of the CuraGen gene

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
31, 32	95124747	331	ATGCCATCCTCAAGGAGC ACGCCATGGAACCAATGAT GTTACATTTCAAAATGCT GGGATAAG[G/A]CTATT AACAAAGGAGGACCTGAGA GTACTCATGGAAAGGAG	G (31)	A (32)	Gly	Asp	NON-CONSERVATIVE		Calpactin		8 of 900	17	Metabolic/endocrine/cardiovascular	
33, 34	91234048	300	GGCCCAAGATGGTGGATG CAACGATGAGCAAGACAAAC ATGGGACACGTT[G/A]CCT CAAGTACCTGCTGTACCTA CAATGCTGCTCTGGCTGGC TGG	G (33)	A (34)	Cys	Tyr	NON-CONSERVATIVE		CD151	2.20E-11	3 of 260		Metabolic/endocrine/cardiovascular	Immunology
35, 36	91234048	965	TGTACCAAGCGCTGGACCA AGCTGCAGCAGGAGTCT[G /C]TGCCTGGCAGCAACA ACTACAGGACCTGGCAGAG CAATGAGTGGATCCG	A (35)	C (36)	His	Pro	NON-CONSERVATIVE		CD151	3.00E-10	6 of 200		Metabolic/endocrine/cardiovascular	Immunology
37, 38	94218949	1446	TAC-G-AGAAGG- CGAC-G-ATG-A- CCGG- ACTGTGTGCCGG G-AG-A-T- CCG[CT]CACAA- CT-CCACGGG- CTGCC-T-GCGGA- T-G-AA-GG-ACCA- GTG-T-G-AC	C (37)	T (38)			Silent-Coding		Clusterin/Apol	8.50E-10	6 of 100	8p12-21	Metabolic/endocrine/cardiovascular	

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SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
39, 40	95351416	1876	GTCAA-TGTCGG- TTTAC-TG- TACACCA-AA- TAAA-CCA- AGCAGG-AC- ATCAA-TGAGC- AA--G(A/G)T- GTTTGTAAG-GGG- TG-CTCC-TG-AA- GG-TG-TCA- TTGACA-GG-T- GCACCC-A-CA- TTCGA-G-TT	A (39)	G (40)	Met	Val	NON- CONSERV ATIVE		SercA1	8.00E-14	3 of 130	12q24.1	Metabolic/endocrine/cardiovascular	
41, 42	97873686	1132	gaagacattggtgctgag gaagcngctatg/tctcag ataagaggagatgtggacct gccccctgagacatctgccc tcttaagccaattgg	G (41)	T (42)	Ala	Ser	NON- CONSERV ATIVE		Valosin-containing protein	5.60E-08	5 of 600	1	Metabolic/endocrine/cardiovascular	
43, 44	95292679	1232	AA-TG-ATAAC-TT- C-TTTG--A-GGGG- AA-GG-A-GCTG-C- GG-C-TG-AAGC-A- GG-AGT-ACTT-C- G-T-GGTGG- CCIG/TJCCA- CGCT-C-CAGGAC- AT-C-AT-CCGC-C- G-C-TTCAAGT-C- G-T-CCAAAG- TTCGG-CTG- CCGGGA-CCC-TG	G (43)	T (44)	Ala	Ser	NON- CONSERV ATIVE		Glycogen Phosphorylase Muscle	2.10E-14	24 of 120	20	Metabolic/endocrine/cardiovascular	

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45, 46	91231553	1353	TGATGGATAATT CCCGGAATGCTC CTTGGCTGGTIT TGGTACGGCTT GCCAATTCTCGT CTGTATGCIAC/A AGTAC-TTTCAA- GGAGATCT-GAAT- CTC-TACTC- TTAT-C-AGGA- TATGG-AACAGA- TGCTAT	A (45)	C (46)			Silent-Coding		Pyruvate dehydrogenase kinase-like protein	6.50E-17	6 of 10	7q21-q22	Metabolic/endocrine/cardiovascular	
47, 48	95108682	2804	CT- GGACCTGATTT- CC- TGACCACAGGC- TCTTGAAG[T/C]- CCCATGTGT- CTTGTGAC-AGA- GG- CCCTAGAGTAA AAGGAGC	T (47)	C (48)			SILENT NONCODING		Galactosidase snailtransferase		7 of 45	3q27	Metabolic/endocrine/cardiovascular	
49, 50	91234048	227	ggggagcctctgcccctg tcctgcgagagagtcgttc cagcccggtt/a/jgccca ggatgggtgagttcaacga gaagaagacacacatgtgac accgttt	T (49)	A (50)			Silent-Coding		CD151	0.23	91 of 250		Metabolic/endocrine/cardiovascular	Immunology
51, 52	94131544	84	ATTAAAGATTTG ATTATTTCAAGTA TGTGAAAACATT CTACAATGGAAA CTC/GTTATTAG ATGCTGCATGTA CTGTGCTATGGA- CCAC-GCACAT- ACAGCC- ATGCTGTTTC- AGAAGAC	C (51)	G (52)			SILENT NONCODING		Rab5-interacting protein		5 of 50	20	Metabolic/endocrine/cardiovascular	

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53, 54	95343665	909	CACCTC-CCT- CACCACACAGGA CCCTGAGT- GAGGA- GGAGGGGCTGGA AACCTGGG[G/C]T GGGTGGCCAAA GGAGAACCCTCAG GCTCCTGGCCCTG GCCAGCTCCTT CTGCCCAAGGT AGCTTAGCCCAT CC	G (53)	C (54)			SILENT NONCODING		Adipocyte-specific protein		3 of 12	3p	Metabolic/endocrine/cardiovascular	
55, 56	97873686	3429	CACAGCCTGCTC CATCTCCAG- TCTGAACAGTTC AGCTA- CAGTCTGACTCT GGACA- GGG[G/T]GTTT- CTGTTGC- AAAAATACAAAA CAAAAGCGATAA AATAAAAG- CGATTTCATT	G (55)	T (56)			SILENT NONCODING		Valosin-containing protein		9 of 30	9p13	Metabolic/endocrine/cardiovascular	Renal Disease
57, 58	97978029	2183	AGCTTGCCTTAA ATTATTTTATAT GACTGTGGTCT CTAGGTAGCC- TTTGGTCTATTGT ACACAAT/CCTC ATTCAATATGTT GCAATTTTGCAA AGAACTTAATAA AATTGTCAGTG	T (57)	C (58)			SILENT NONCODING		Medium Chain Acyl CoA Dehydrogenase		4 of 11	1p31 1-31 3	Metabolic/endocrine/cardiovascular	
59, 60	95289295	3121	aaggccaccatgcatttattta tcgctttg[c/gap]ggaga caagcaccagcccgagt tgctggggagctccatta actagag	C (59)	gap (60)			SILENT NONCODING		Creatine Kinase Muscle		25 of 90	19q13 2	Metabolic/endocrine/cardiovascular	

TABLE 1. BLASTX analysis of the CuratGen sequence

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuratGen gene	Name of protein identified following a BLASTX analysis of the CuratGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
61, 62	cg42709360	955	GGCCGGGGAGTG GCGATGGTGACT GC/C/TGTGGCTG CCGCTCTGGCTG CCCACCG	C (61)	T (62)			Silent-Coding	kinase	Human Gene Similar to SWISSPROT-ID P17709 GLUCOKINASE (EC 2 7 1 2) (GLUCOSE KINASE) (GLK) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 500 aa Hs01pels SWISSPROT-ID P17709 GLUCOKINASE (EC 2 7 1 2) (GLUCOSE KINASE) (GLK) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 500 aa	4.10E-39		5 (5p35.2)	Metabolic/endocrine/cardiovascular	
63, 64	cg43920091	21	GGCCCTTAGGTT GTCTTGAGAGGG GGATGCCCTGTG /gap/CCCTGGCTC ACTGTGACCTG- CTCCTGCCACG- TGC	G (63)	gap (64)			SILENT-NONCODING	ATPase associated	Human Gene SWISSPROT-ID Q13608 PEROXISOME ASSEMBLY FACTOR-2 (PAF-2) (PEROXISOMAL-TYPE ATPASE 1) (PEROXIN-6) - HOMO SAPIENS (HUMAN), 980 aa	0		6 (6p21.1)	Metabolic/endocrine/cardiovascular	
65, 66	cg44913012	75	GGATCATAGGC AAATGTTTAAT- TAAAT/gap/CTGC T-CA-TATGCAC- ATCTGAAAGC- ATGA	AATT (65)	gap (66)			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID Q01813 PHOSPHOFRUCTOKINASE, TYPE C (EC 2 7 1 11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE) (ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	6.0	4bp deletion, 8 of 60	10 (10p15.3)	Metabolic/endocrine/cardiovascular	
67, 68	cg44913012	142	ATGAGACACA- CTCC- ACAGACAGCAG CACTGG-A/G/G- CTGGTGG- GGCAGATGGCA CTCGCGATTAG GT	A (67)	G (68)			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID Q01813 PHOSPHOFRUCTOKINASE, TYPE C (EC 2 7 1 11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE) (ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	6.0	27 of 75	10 (10p15.3)	Metabolic/endocrine/cardiovascular	

Variable	Unit	Mean	Standard Deviation	Minimum	Maximum
Age	Years	35.2	10.5	20	55
Height	Centimeters	175.8	7.2	160	190
Weight	Kilograms	72.5	12.1	55	100
Heart Rate	Beats per minute	72.1	10.3	60	90
Blood Pressure	mmHg	120/80	15/10	110/70	130/90
Cholesterol	mg/dL	185	45	140	240
Glucose	mg/dL	95	15	70	120
Hemoglobin	g/dL	14.5	1.2	13.0	16.0
Hematocrit	%	42.5	3.5	38.0	47.0
White Blood Cells	mm ³	7,500	1,500	6,000	9,000
Platelets	mm ³	250,000	50,000	200,000	300,000

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69, 70	cg44913012	134	ATCTGAAGC- ATGAGACACA- CTCC- ACAGACAGCAC[G/A]CACTGG-AG- CTGGTGG- GGCAGATGGGCA- CTCGC	G (69)	A (70)			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID Q01813 640 PHOSPHOFRUCTOKINASE, TYPE C (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	6.0	15 of 75	10 (10p15.3)	Metabolic/endocrine/ neurocardiovascular	
71, 72	cg44913012	1530	CTGTCC-AG-CC-G- A-TTTT-CTTT- GATCT-GGCCCTT- GG-C- [A/G]AAGCC-G-T- CA-A-A-GCCAT- CA-TAGATGG-CG- AG-CAT-CCTG	G (71)	T (72)			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID Q01813 640 PHOSPHOFRUCTOKINASE, TYPE C (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	6.0	36 of 200	10 (10p15.3)	Metabolic/endocrine/ neurocardiovascular	
73, 74	cg44913012	1630	TGGCGTCGGCA AT-GCCC-ACCG- C-ACA-G- CTGAGC-G-T- ACGCCT/CJCGCT T-CA-TCC-CA-GC- CGCGGGTCCCC C-ACGTTGATGA	G (73)	T (74)			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID Q01813 640 PHOSPHOFRUCTOKINASE, TYPE C (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	6.0	35 of 200	10 (10p15.3)	Metabolic/endocrine/ neurocardiovascular	
75, 76	94238747	1638	TTCT- CCGGGCCCACTG GATGGTGA- GGGGGT-- CCCGGTGCCAG- GTT/CJGGGGCG GC- AGGCTCCACTGG GCACCTTGCTGAG A-G- CTTGGCGGCTT- GAGCAGCGCTG GTC	T (75)	C (76)			SILENT- NONCODI NG		CD98		41 of 50	16q24.3	Metabolic/endocrine/ neurocardiovascular	Immunology

TABLE 1. BLASTX analysis of the CuraGen sequence

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77, 78	95072341	286	TTTATACATAC AT-ACAATTA- TCA-GG-AATG-C- AAAAAAAAAA[A] gapICATAAATAAT GCCCATTTT-A- CA-GG-TG-A-C-A- TTTTAAA-C-AA- TG-AAAAA-C- ACCAACGG	A (77)	gap (78)			SILENT NON-CODING	Kinase	sgk		46 of 200	5	Metabolic/endocrine/cardiovascular	Renal Disease
79, 80	95308696	445	AAAGGTGTGGAT G-AAGCAACCAT- CATTGACA- TTCTA-CTA-AG- CGAAACAATGCA [CT]AGCG- TCAACA- GATCAAAGCAGC ATAT-C-T-CC	C (79)	T (80)	Gln	STOP	Termination		lipocortin 1	1.60E-07	2 of 150	9	Metabolic/endocrine/cardiovascular	
81, 82	sg43064060	805	AGAAACAA- ATGCCAG-TATTG- TC-GATTT- CACAAAGTGCCTT TCTGTCGGGATG TCACACAAACGiga pGTAGJCGATTCTG TTTGGACGAA- TGCCAAGATCTG AGAAAGCAAAAC TGAAAGCAGAAA	gap (81)	GTAG (82)			Frameshift	nuc_recept	Human Gene SWISSPROT-ID Q07869 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA) - HOMO SAPIENS (HUMAN), 468 aa Ipeis SPTREMBL- ID Q16241 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA - HOMO SAPIENS (HUMAN), 468 aa (fragment)	4.10E-254	4bp insertion polymorphism 3 of 10	22	Metabolic/endocrine/cardiovascular	
83, 84	sg106711057	775	CGAT-GG-CT-T- GG-TCTT-A- AGGTGCCT-A-A- CCTCCTCT- GCAGCTT/AJTT- CTCAAACT-CAG- CCTGAGA- CATCCT-GG-C-C- GACTT- GCAAGAACT- CCA	T (83)	A (84)	Lys	Asn	NON-CONSERVATIVE	Peptide hormone	Acyl CoA Binding Protein		2 of 130	6q13-15	Metabolic/endocrine/cardiovascular	CNS Disorders

TABLE 1. BLASTX analysis of the CuraGen database for the identification of proteins identified following a BLASTX analysis of the CuraGen database.

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen database	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
85, 86	cg106711057	477	AAGGCATGTC-TC-AG-TT1AGG-ATAACACACATGGCACAG1AA-CC-AAATCCAG-TC1CT-CATATCCCG(C/T)ATTTTCTTTAGCTCTTCTACTTGTGATGTAAG	C (85)	T (86)	Tyr	Cys	NON-CONSERVATIVE	Peptide hormone	Acy CoA Binding Protein		3 of 180	6q13-15	Metabolic/endocrine/cardiovascular	CNS Disorders
87, 88	cg108881866	170	TTCAGCT-GCACATGAATAGAACAGCAAT-G-AGAGCCAGTCAGAA-GG-AC1TTGAAAA-TTCAAT[G/A]AATCAAGT-GAAACTC-TT-GAAAA-GGAT-CCAGGAAA-CGAA-GTGA-AGCTAAACTCTACGCCATATAAGCAGGCC	G (87)	A (88)	Met	Ile	Conservative	Peptide hormone	DBI-related Protein		10 of 60	6p24 1-25 3	Metabolic/endocrine/cardiovascular	Oncology
89, 90	cg108881866	741	G-CTGCC-AG-C-AA-GG-ATG-A-CTCAAT-CATCACTG-TTTT-AAC-AGG-AA-A-TGGTGA-CT[A/G]TT-ACA-G-TA-G-T-G-GGAA-TGA-T-CTG-A-CTAAC-TT-C-AC-TG-ATA-TT-CC-CC-C-T-G-GT-GG-AG-T-AG-AG-GAG	A (89)	G (90)	Cys	Tyr	NON-CONSERVATIVE	Peptide hormone	DBI-related Protein		3 of 200	6p24 1-25 3	Metabolic/endocrine/cardiovascular	Oncology

TABLE 1

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
91, 92	cg108881866	851	ATA-TT-CC-CC-C-T- T-G-GT-GG-AG-T- AG-AG-GAG- AAAG-CTA- AAAATA[A/G]TG- CC-GT-TTTA-C- TGAGGGAA-T-TT- G--T- GGGCTGTTTAT AGATTTT	A (91)	G (92)	Asn	Ser	NON- CONSERV ATIVE	Peptide hormone	DBI-related Protein		3 of 200	6p24 1:25 3	Metabolic/endocrine/cardiovascular	Oncology
93, 94	cg108881866	1309	C-AC-TTTT-C-AG- AAAGAAG- TCTGGA-- CCAGGC-T-GAA- GGCA-TTTC- AAAGCTT-- CCCC-AAAT- G[C/T] CTG-AG- AATT C-AAAAG- AGG-TAAT-CA- GG-AAAAG- AGAGAG-A-G- AAAAACTACAC- GCT-GTT-AATG-C- TGA-AGAAATG- CAAT-G-T-CC- TTCAG	C (93)	T (94)	Val	Ala	Conservative	Peptide hormone	DBI-related Protein		8 of 50	6p24 1:25 3	Metabolic/endocrine/cardiovascular	Oncology

TABLE 1

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
95, 96	cg108881866	1404	AAATTTC-AAAAG- AGG-TAAT-CA- GG-AAAAG- AGAGAG-A-G- AAAAACTACAC- GCT-GTT-AATG-C- TGA- AGAAATG[T/G] AAT-G-T-CC- TTCAG-GG- AAGATGG-CTATC- AGAT-GAA- TGCACAAAT- GCTGTGGTG- AACTT-CTTAT- CCAGAAA- TCAAA	T (95)	G (96)	Cys	Trp	NON- CONSERV ATIVE	Peptide hormone	DBI-related Protein		2 of 40	6p24.1:25.3	Metabolic/endocrine/cardiovascular	Oncology